(1) GENERAL INFORMATION

(i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne;
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Fulbright & Jaworski LLP
     (B) STREET: 666 Fifth Avenue
     (C) CITY: New York City
     (D) STATE: New York
     (E) COUNTRY; USA
     (F) ZIP: 10103

(v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
     (B) COMPUTER: IBM
     (C) OPERATING SYSTEM: PC-DOS
     (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: 08/819,669
     (B) FILING DATE: 17-March-1997
     (C) CLASSIFICATION: 435

(vii) PRIOR APPLIATION DATA:
     (A) APPLICATION NUMBER: 08/142,368
     (B) FILING DATE: 02-MAY-1994

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: PCT/US92/04354
     (B) FILING DATE: 22-MAY-1992

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/807,043
     (B) FILING DATE: 12-DECEMBER-1991

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/764,364
     (B) FILING DATE: 23-SEPTEMBER-1991

(vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: 07/728,838
     (b) FILING DATE: 9-JULY-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/705,702
         (B) FILING DATE: 23-May-1991

      (viii) ATTORNEY/AGENT INFORMATION:
         (A) NAME: Hanson, Norman D.
         (B) REGISTRATION NUMBER: 30,946
         (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US

      (ix) TELECOMMUNICATION INFORMATION:
         (A) TELEPHONE: (212)318-3168
         (B) TELEFAX: (212)752-5958

(2)   INFORMATION FOR SEQUENCE ID NO: 1:
      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 462 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG   60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT   120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG   180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC   240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT   300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG CATGCATTGT   360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT   420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC   462

(2)   INFORMATION FOR SEQUENCE ID NO: 2:
      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 675 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT   48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
                 5   10   15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA   96

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Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
        20                      25                      30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA        144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
        35                      40                      45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG        192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
        50                      55                      60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC        240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65                      70                      75                      80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC        288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
                        85                      90                      95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
                100                     105                     110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG        384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
                115                     120                     125
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG        432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
        130                     135                     140
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG        480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
145                     150                     155                     160
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC        528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
                165                     170                     175
CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT        576
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
                180                     185                     190
GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG        624
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
                195                     200                     210
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT        672
Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
220                     225                     230                     235

TAG                                                                    675
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(2)   INFORMATION FOR SEQUENCE ID NO: 3:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 228 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

576670.1

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GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT          60
TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT         120
TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACTTT CATATGATAC         180
ATAGGATTAC ACTTGTACCT GTTAAAAATA AAAGTTTGAC TTGCATAC                      228
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(2)   INFORMATION FOR SEQUENCE ID NO: 4:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1365 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:


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ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT          50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT         100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG         150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT         200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG         350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG         400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT         450
ACCCTTTGTG CC                                                  462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA         504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG         546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC         588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC         630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC         672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG         714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC         756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT         798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA         840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA         882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT         924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT         966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG        1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT        1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG GAG GAG        1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT        1134
TAG                                                           1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG        1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA        1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT        1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT        1337
GTTAAAAATA AAGTTTGAC TTGCATAC                                 1365
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(2)   INFORMATION FOR SEQUENCE ID NO: 5:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 4698 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA

576670.1

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GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT         100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG         150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT         200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA         250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT         300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCCTTT GCTCTCCCAG         350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG         400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT         450
ACCCTTTGTG CC                                                  462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA        504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG        546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC        588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC        630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC        672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG        714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC        756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT        798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA        840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA        882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T                  916
GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA         966
CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC        1016
TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC        1066
CCCCACTCCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC        1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC        1166
TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC        1216
TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCCTCCCC TTCCTGTTCC        1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT        1316
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT        1366
TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT        1416
CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTCGGG        1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT        1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTTT TTTTTTTTTT        1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC        1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CCTGCCTCTG        1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG        1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT        1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT        1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC        1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT        1916
GCCCCGTTCC CCTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC        1966
AGCTCACCTT TTTGTTTGTT TGGTTGTTTG GTTGTTTGGT TTGCTTTTTT        2016
TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCCC TCCGGCTTCC        2066
CCTCTGTGTG CCTTTCCTGT TCCCTCCCCC TCGCTGGCTC CCCCTCCCTT        2116
TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT.       2166
CTTTTCTAGA CTCCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT        2216
CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC        2266
CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT        2316
TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG        2366
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GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC          2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT          2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT          2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA          2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT          2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC          2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC          2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC          2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC          2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC          2866
ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAAA ATCAGCAGGA          2916
AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC          2966
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT          3016
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG          3066
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA          3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG          3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA          3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA          3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT          3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG                     3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT         3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT         3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA         3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA         3522
GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC         3564
TTC TCA CCT TAG                                                3576
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GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA          3676
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CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT          3776
GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA          3826
GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG          3876
TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT          3926
TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG          3976
TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAGAG ATGAAAATCT          4026
CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT          4076
TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA          4126
AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA          4176
GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA          4226
GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC          4276
CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC          4326
ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT          4376
ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA          4426
AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC          4476
AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT          4526
TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA          4576
TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT          4626
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA          4676
AATAAAAGTT TGACTTGCAT AC                                       4698
```

(2)   INFORMATION FOR SEQUENCE ID NO: 6:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
                5

(2)   INFORMATION FOR SEQUENCE ID NO: 7:
       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2419 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG   50
GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC   100
TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG   150
GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT   200
TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT   250
·GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA   300
CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT   350
CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC   400
TTCCTCCTTC AGGTTTTCAG GGGACAGGCC AACCCAGAGG ACAGGATTCC   450
CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG   500
TTAGAGTCTC CAAGGTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT   550
CTCTCCCCAG GCCTGTGGGT CTTCATTGCC CAGCTCCTGC CCACACTCCT   600
GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC   650
ACTGCAAGCC TGAGGAAGCC CTTGAGGCCC AACAAGAGGC CCTGGGCCTG   700
GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC   750
CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC   800
AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA   850
CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG   900
TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT   950
TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG   1000
GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA   1050
GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG   1100
TGAAGGAAGC AGACCCCACC GGCCACTCCT ATGTCCTTGT CACCTGCCTA   1150
GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC   1200
AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GGCGGCCATG   1250
CTCCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT   1300
GGGAGGGAGC ACAGTGCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA   1350
TTTGGTGCAG GAAAAGTACC TGGAGTACGG CAGGTGCCGG ACAGTGATCC   1400

     576670.1

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CGCACGCTAT GAGTTCCTGT GGGGTCCAAG GGCCCTCGCT GAAACCAGCT          1450
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TTCTTCCCAT CCCTGCGTGA AGCAGCTTTG AGAGAGGAGG AAGAGGGAGT          1550
CTGAGCATGA GTTGCAGCCA AGGCCAGTGG GAGGGGGACT GGGCCAGTGC          1600
ACCTTCCAGG GCCGCGTCCA GCAGCTTCCC CTGCCTCGTG TGACATGAGG          1650
CCCATTCTTC ACTCTGAAGA GAGCGGTCAG TGTTCTCAGT AGTAGGTTTC          1700
TGTTCTATTG GGTGACTTGG AGATTTATCT TTGTTCTCTT TTGGAATTGT          1750
TCAAATGTTT TTTTTAAGG GATGGTTGAA TGAACTTCAG CATCCAAGTT          1800
TATGAATGAC AGCAGTCACA CAGTTCTGTG TATATAGTTT AAGGGTAAGA          1850
GTCTTGTGTT TTATTCAGAT TGGGAAATCC ATTCTATTTT GTGAATTGGG          1900
ATAATAACAG CAGTGGAATA AGTACTTAGA AATGTGAAAA ATGAGCAGTA          1950
AAATAGATGA GATAAAGAAC TAAAGAAATT AAGAGATAGT CAATTCTTGC          2000
CTTATACCTC AGTCTATTCT GTAAAATTTT TAAAGATATA TGCATACCTG          2050
GATTTCCTTG GCTTCTTTGA GAATGTAAGA GAAATTAAAT CTGAATAAAG          2100
AATTCTTCCT GTTCACTGGC TCTTTTCTTC TCCATGCACT GAGCATCTGC          2150
TTTTTGGAAG GCCCTGGGTT AGTAGTGGAG ATGCTAAGGT AAGCCAGACT          2200
CATACCCACC CATAGGGTCG TAGAGTCTAG GAGCTGCAGT CACGTAATCG          2250
AGGTGGCAAG ATGTCCTCTA AAGATGTAGG GAAAAGTGAG AGAGGGGTGA          2300
GGGTGTGGGG CTCCGGGTGA GAGTGGTGGA GTGTCAATGC CCTGAGCTGG          2350
GGCATTTTGG GCTTTGGGAA ACTGCAGTTC CTTCTGGGGG AGCTGATTGT          2400
AATGATCTTG GGTGGATCC                                            2419
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(2)   INFORMATION FOR SEQUENCE ID NO: 8:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 5674 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-1 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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CCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT            50
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AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG          150
ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT          200
CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG          250
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AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG          500
AGGGCTGAGG GTCCCTAAGA CCCCACTCCC GTGACCCAAC CCCCACTCCA          550
ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCATT CCAACCCCCA          600
CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC          650
ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC          700
CAGGCAGGAT CCGGTTCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC          750
GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG          800
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CCTTGAGAGA CACCAGGTTC TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC       1050
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GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC       1150
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CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA       1250
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(2)   INFORMATION FOR SEQUENCE ID NO: 9:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 4157 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-2 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:


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GCTCAGTCGC CACCACCTCA CCCCGCCACC CCCGCCGCT TTAACCGCAG          350
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TTC TCG ACT ACC ATC AAC TAC ACT CTT TGG AGA CAA TCC GAT        2849
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(2) INFORMATION FOR SEQUENCE ID NO: 10:
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        (A) LENGTH: 662 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
    (ix) FEATURE:
        (A) NAME/KEY: MAGE-21 gene
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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(2) INFORMATION FOR SEQUENCE ID NO: 11:
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        (A) LENGTH: 1640 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA to mRNA
    (ix) FEATURE:
        (A) NAME/KEY: cDNA MAGE-3
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA         213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG         255
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TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC         339
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(2) INFORMATION FOR SEQUENCE ID NO: 12:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 943 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-31 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

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TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC               350
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576670.1

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CTCCCGCCTG TTGCCCTGAC CAGAGTCATC   580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA   622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG   664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT   706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC   748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC   790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT   832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC   874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG   916
GTG GCC AAG TTG GTT CAT TTT CTG CTC   943

(2)   INFORMATION FOR SEQUENCE ID NO: 13:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2531 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-4 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG   50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC   100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG   150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT   200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT   250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA   300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT   350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA   400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC   450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT   500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC   550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG   600
CCTGCTGCCC TGACCAGAGT CATC   624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA   666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA   708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC   750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT   792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT   834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC   876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC   918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC   960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA   1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC   1044

```
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA          1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG          1128
GAA GTG GAC CCC GCC AGC AAC ACC TAC ACC CTT GTC ACC TGC          1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC          1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT          1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG          1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT          1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG          1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT          1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT          1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC          1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA          1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                          1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC          1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC          1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT          1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT          1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT          1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG          1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG          1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT          1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA          2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG          2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA          2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC          2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA          2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT          2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT          2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA          2378
AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC          2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC          2478
TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT          2528
GGG                                                             2531
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(2)   INFORMATION FOR SEQUENCE ID NO: 14:
      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2531 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS:single
            (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
            (A) NAME/KEY: MAGE-41 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:


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GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG          50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC          100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG          150
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GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT        200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT        250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA        300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT        350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA        400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC        450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT        500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC        550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG        600
CCTGCTGCCC TGAGCAGAGT CATC                                    624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA       666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCG       708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC TCC       750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT       792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT       834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC       876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC       918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC       960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA      1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC      1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT GTG ATC TTC GGC AAA      1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT GGC ATT GAC GTG AAG      1128
GAA GTG GAC CCC ACC AGC AAC ACC TAC ACC CTT GTC ACC TGC      1170
CTG GGC CTT TCC TAT GAT GGC CTG CTG GGT AAT AAT CAG ATC      1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC GTC CTG GGC ACA ATT      1254
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG GAA ATC TGG GAG      1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT      1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG      1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT      1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT      1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC      1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA      1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA                      1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC       1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC       1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT       1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT       1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACTTCA GCATCCAAGT       1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG       1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG       1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT       1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCCGCC TTATGCCTCA       2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCCTTGG       2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA       2128
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATCTGCTCTG TGGAAGGCCC       2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA       2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT       2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GCTCCAGGT        2328
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGGCCTTTTG GCTTTGGGA        2378
AACTCCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC       2428
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCCCAGATTG GAAAAGTTGC       2478
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT       2528
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(2)   INFORMATION FOR SEQUENCE ID NO: 15:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1068 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: cDNA to mRNA
       (ix) FEATURE:
           (A) NAME/KEY: cDNA MAGE-4
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

   G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA   40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG   82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA   124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT   166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT   208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC   250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG   292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC   334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG   376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT   418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC   460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG   502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT   544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG   586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA   628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC   670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG   720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG   770
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTC TTAGTAGTGG   820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA   870
ATTGTTGAAA TGTTCCTTTT AATGGATGGT TGAATTAACT TCAGCATCCA   920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT   970
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT   1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC   1068

(2)   INFORMATION FOR SEQUENCE ID NO: 16:
       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 2226 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: genomic DNA
       (ix) FEATURE:
           (A) NAME/KEY: MAGE-5 gene
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

576670.1

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GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG        50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC       100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG       150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT       200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC       250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC       300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG       350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT       400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG       450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG       500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA       550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC       600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC            644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA       686
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG       728
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA       770
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA       812
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC       854
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG       896
TGG CTG ACT TGA                                             908
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT CACAAAGGCA       958
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TCCTGAGAT       1008
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA      1058
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA      1108
CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG CCCAAGACGG      1158
GCCTCCTGAT AATCGTCTTG GCATGATTG CAATGGAGGG CAAATGCGTC       1208
CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG TGTATGTTGG      1258
GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC ACCCAAGATT      1308
TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCCAG CAGTGATCCC      1358
ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG CTTGAAAGTA      1408
CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT CCTACCCATC      1458
CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC TGAGCATGAG      1508
CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA CCTTCCAGGG      1558
CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG CCCATTCTTC      1608
TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT TCTGTTCTAT      1658
TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT GTTCAAATGT      1708
TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT TTATGAATGA      1758
CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA AGAGTCTTGT      1808
TTTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT GGGACATAGT      1858
TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA GCAGTAAAAC      1908
TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT ATACTCAGTC      1958
TATTCGGTAA AATTTTTTTT AAAAAATGTG CATACCTGGA TTTCCTTGGC      2008
TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA TTCTCCCTGT      2058
TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC TGTGGAAGGC      2108
CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA CCCCTACCCA      2158
CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG GTGGAGAGAT      2208
GCCCTCTAAG ATGTAGAG                                        2226
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(2)   INFORMATION FOR SEQUENCE ID NO: 17:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 2305 base pairs
           (B) TYPE; nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-51 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG   50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC CAGCCTACCC   100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT GCACCCTGAG   150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC ACTGAGGCCT   200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA TGCAGACGTC   250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT GGCCCCCATC   300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC CTCTCTACTG   350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT GAGGTGCCCT   400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA GGATCACCAG   450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG   500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT TTTTAGCTGA   550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC   600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC   644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA   686
GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG TGG GTG TGC   728
AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT CCT CCT CCT   770
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC CTG CTG CTG   812
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG CCT CCG CCA   854
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC AAT CCA TTA   896
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA GCA CCT CCC   938
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA GTA AGA AGG   980
TGG CTG ACT TGA   992
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT CACAAAGGCA   1042
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT TCCTGAGAT   1092
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC ATTGACGTGA   1142
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC CTGCCTGGGA   1192
CTCCTATGAT GGCTGGTGG TTTAATCAGA TCATGCCCAA GACGGGCCTC   1242
CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT GCGTCCCTGA   1292
GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT GTTGGGAGGG   1342
AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA AGATTTGGTG   1392
CAGGAAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA TCCCATATGC   1442
TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA AGTACTGGAG   1492
CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCTACC CATCCCTGCA   1542
TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA TGAGCTGCAG   1592
CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC AGGGCTCCGT   1642
CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT CTTCTCTCTT   1692
TGAAGAGAGC AGTCAACATT CTTAGTAGTG GGTTTCTGTT CTATTGGATG   1742
ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA ATGTTCCTTT   1792
TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA ATGACAGTAG   1842

576670.1

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TCACACATAG TGCTGTTTAT ATAGTTTAGG AGTAAGAGTC TTGTTTTTTA          1892
TTCAGATTGG GAAATCCATT CCATTTTGTG AATTGGGACA TAGTTACAGC          1942
AGTGGAATAA GTATTCATTT AGAAATGTGA ATGAGCAGTA AAACTGATGA          1992
GATAAAGAAA TTAAAAGATA TTTAATTCTT GCCTTATACT CAGTCTATTC          2042
GGTAAAATTT TTTTTTAAAA ATGTGCATAC CTGGATTTCC TTGGCTTCTT          2092
TGAGAATGTA AGACAAATTA AATCTGAATA AATCATTCTC CCTGTTCACT          2142
GGCTCATTTA TTCTCTATGC ACTGAGCATT TGCTCTGTGG AAGGCCCTGG          2192
GTTAATAGTG GAGATGCTAA GGTAAGCCAG ACTCACCCCT ACCCACAGGG          2242
TAGTAAAGTC TAGGAGCAGC AGTCATATAA TTAAGGTGGA GAGATGCCCT          2292
CTAAGATGTA GAG                                                  2305
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(2)   INFORMATION FOR SEQUENCE ID NO: 18:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 225 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: cDNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-6 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

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TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG          42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC          84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC          126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC          168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC          210
TGT GCC CCT GAG GAG                                              225
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(2)   INFORMATION FOR SEQUENCE ID NO: 19:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1947 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: genomic DNA
      (ix) FEATURE:
           (A) NAME/KEY: MAGE-7 gene
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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TGAATGGACA ACAAGGGCCC CACACTCCCC AGAACACAAG GGACTCCAGA           50
GAGCCCAGCC TCACCTTCCC TACTGTCAGT CCTGCAGCCT CAGCCTCTGC          100
TGGCCGGCTG TACCCTGAGG TGCCCTCTCA CTTCCTCCTT CAGGTTCTCA          150
GCGGACAGGC CGGCCAGGAG GTCAGAAGCC CCAGGAGGCC CCAGAGGAGC          200
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ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT          250
GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG          300
GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA          350
CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG          400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG          450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA          500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA          550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA          600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC          650
TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA                          685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT          727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA          769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT          811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC          853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA          895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC          937
AGA GCA TGC CCG AGA CCG GCC TTC TGA                              964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG         1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT         1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC         1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT         1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG         1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG         1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC         1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC         1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT         1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG         1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC         1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT         1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG         1614
GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTTAT         1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG         1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG         1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG         1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA         1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA         1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG                           1947


(2)   INFORMATION FOR SEQUENCE ID NO: 20:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:  1810 base pairs
          (B) TYPE:   nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY:  linear
     (ii) MOLECULE TYPE:  genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY:  MAGE-8 gene
     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 20:
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GAGCTCCAGG AACCAGGCTG TGAGGTCTTG GTCTGAGGCA GTATCTTCAA        50
TCACAGAGCA TAAGAGGCCC AGGCAGTAGT AGCAGTCAAG CTGAGGTGGT       100
GTTTCCCCTG TATGTATACC AGAGGCCCCT CTGGCATCAG AACAGCAGGA       150
ACCCCACAGT TCCTGGCCCT ACCAGCCCTT TTGTCAGTCC TGGAGCCTTG       200
GCCTTTGCCA GGAGGCTGCA CCCTGAGATG CCCTCTCAAT TTCTCCTTCA       250
GGTTCGCAGA GAACAGGCCA GCCAGGAGGT CAGGAGGCCC CAGAGAAGCA       300
CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA       350
CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT       400
CAATTGCCCA GCTCCGGCCC ACACTCTCCT GCTGCCCTGA CCTGAGTCAT       450
C                                                           451
ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA       493
GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG       535
CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC       577
TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT       619
GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT       661
TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT       703
GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC       745
CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT       787
GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA       829
TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG       871
AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC       913
AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT       955
GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC       997
ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT      1039
CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC      1081
ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC      1123
TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA                  1156
TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG      1206
AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT      1256
CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG      1306
CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA      1356
TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT      1406
TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG      1456
GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCCT GCTCTGTTAC      1506
ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA      1556
GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC      1606
AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG      1656
AATTGTTCCA ATGTTCCTTC TAATGGATGG TGTAATGAAC TTCAACATTC      1706
ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTTATA TAGTTTAGGA      1756
GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA      1806
ATTC                                                       1810
```

(2)   INFORMATION FOR SEQUENCE ID NO: 21:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1412 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
        (ii) MOLECULE TYPE: genomic DNA
        (ix) FEATURE:

```
        (A) NAME/KEY:  MAGE-9 gene
    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 21:


TCTGAGACAG TGTCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC          50
AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT         100
GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG         150
TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC         200
TCTCACTTCC TCCCTCAGGT TCTCGGGACA GGCTAACCAG GAGGACAGGA         250
GCCCCAAGAG GCCCCAGAGC AGCACTGACG AAGACCTGTA AGTCAGCCTT         300
TGTTAGAACC TCCAAGGTTC GGTTCTCAGC TGAAGTCTCT CACACACTCC         350
CTCTCTCCCC AGGCCTGTGG GTCTCCATCG CCCAGCTCCT GCCCACGCTC         400
CTGACTGCTG CCCTGACCAG AGTCATC                                  427
ATG TCT CTC GAG CAG AGG AGT CCG CAC TGC AAG CCT GAT GAA        469
GAC CTT GAA GCC CAA GGA GAG GAC TTG GGC CTG ATG GGT GCA        511
CAG GAA CCC ACA GGC GAG GAG GAG GAG ACT ACC TCC TCC TCT        553
GAC AGC AAG GAG GAG GAG GTG TCT GCT GCT GGG TCA TCA AGT        595
CCT CCC CAG AGT CCT CAG GGA GGC GCT TCC TCC TCC ATT TCC        637
GTC TAC TAC ACT TTA TGG AGC CAA TTC GAT GAG GGC TCC AGC        679
AGT CAA GAA GAG GAA GAG CCA AGC TCC TCG GTC GAC CCA GCT        721
CAG CTG GAG TTC ATG TTC CAA GAA GCA CTG AAA TTG AAG GTG        763
GCT GAG TTG GTT CAT TTC CTG CTC CAC AAA TAT CGA GTC AAG        805
GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGC GTC ATC AAA        847
AAT TAC AAG CGC TAC TTT CCT GTG ATC TTC GGC AAA GCC TCC        889
GAG TTC ATG CAG GTG ATC TTT GGC ACT GAT GTG AAG GAG GTG        931
GAC CCC GCC GGC CAC TCC TAC ATC CTT GTC ACT GCT CTT GGC        973
CTC TCG TGC GAT AGC ATG CTG GGT GAT GGT CAT AGC ATG CCC       1015
AAG GCC GCC CTC CTG ATC ATT GTC CTG GGT GTG ATC CTA ACC       1057
AAA GAC AAC TGC GCC CCT GAA GAG GTT ATC TGG GAA GCG TTG       1099
AGT GTG ATG GGG GTG TAT GTT GGG AAG GAG CAC ATG TTC TAC       1141
GGG GAG CCC AGG AAG CTG CTC ACC CAA GAT TGG GTG CAG GAA       1183
AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCG       1225
CAC TAC GAG TTC CTG TGG GGT TCC AAG GCC CAC GCT GAA ACC       1267
AGC TAT GAG AAG GTC ATA AAT TAT TTG GTC ATG CTC AAT GCA       1309
AGA GAG CCC ATC TGC TAC CCA TCC CTT TAT GAA GAG GTT TTG       1351
GGA GAG GAG CAA GAG GGA GTC TGA                               1375
GCACCAGCCG CAGCCGGGGC CAAAGTTTGT GGGGTCA                      1412



(2)   INFORMATION FOR SEQUENCE ID NO: 22:
      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH:  920 base pairs
          (B) TYPE:   nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY:  linear
      (ii) MOLECULE TYPE:  genomic DNA
      (ix) FEATURE:
          (A) NAME/KEY:  MAGE-10 gene
      (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 22:
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ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC ACCTACCCTA        50
CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT GAGGAGCCAT       100
CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG CAAGAGGTCA       150
AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA CCTGTAAGTT       200
GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTG GCCACTTACA       250
CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA AGTCCTGCCC       300
ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC                         333
ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATG CCT GAA GAA       375
GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC GAG GGT GCA       417
CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA TCA TCC ACT       459
TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC       501
TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC       543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC       585
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT       627
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA       669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT       711
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT       753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG       795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT       837
GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC       879
ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC        920
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(2)   INFORMATION FOR SEQUENCE ID NO: 23:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1107 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
     (ii) MOLECULE TYPE: genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY: MAGE-11 gene
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:


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AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT        50
CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT       100
CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG       150
GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG       200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG       250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC       300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC       350
ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC       400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC       450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA GGAGGGGCC AAGTACCTCG        500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA       550
GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT       600
GATCACAAAG GCAGAA                                            616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT       658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT       700
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GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT                     742
GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG                     784
TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA                     826
GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA                     868
GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT                     910
GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT                     952
ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG                     994
GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT                    1036
CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG                    1078
TAC ATA GCC AAT GCC AAT GGG AGG GAT CC                                     1107
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TCTGTCTGCA TATGCCTCCA CTTGTGTGTA GCAGTCTCAA ATGGATCTCT          50
CTCTACAGAC CTCTGTCTGT GTCTGGCACC CTAAGTGGCT TTGCATGGGC         100
ACAGGTTTCT GCCCCTGCAT GGAGCTTAAA TAGATCTTTC TCCACAGGCC         150
TATACCCCTG CATTGTAAGT TTAAGTGGCT TTATGTGGAT ACAGGTCTCT         200
GCCCTTGTAT GCAGGCCTAA GTTTTTCTGT CTGCTTAACC CCTCCAAGTG         250
AAGCTAGTGA AAGATCTAAC CCACTTTTGG AAGTCTGAAA CTAGACTTTT         300
ATGCAGTGGC CTAACAAGTT TTAATTTCTT CCACAGGGTT TGCAGAAAAG         350
AGCTTGATCC ACGAGTTCAG AAGTCCTGGT ATGTTCCTAG AAAG              394
ATG TTC TCC TGG AAA GCT TCA AAA GCC AGG TCT CCA TTA AGT        436
CCA AGG TAT TCT CTA CCT GGT AGT ACA GAG GTA CTT ACA GGT        478
TGT CAT TCT TAT CCT TCC AGA TTC CTG TCT GCC AGC TCT TTT        520
ACT TCA GCC CTG AGC ACA GTC AAC ATG CCT AGG GGT CAA AAG        565
AGT AAG ACC CGC TCC CGT GCA AAA CGA CAG CAG TCA CGC AGG        604
GAG GTT CCA GTA GTT CAG CCC ACT GCA GAG GAA GCA GGG TCT        646
TCT CCT GTT GAC CAG AGT GCT GGG TCC AGC TTC CCT GGT GGT        688
TCT GCT CCT CAG GGT GTG AAA ACC CCT GGA TCT TTT GGT GCA        730
GGT GTA TCC TGC ACA GGC TCT GGT ATA GGT GGT AGA AAT GCT        772
GCT GTC CTG CCT GAT ACA AAA AGT TCA GAT GGC ACC CAG GCA        814
GGG ACT TCC ATT CAG CAC ACA CTG AAA GAT CCT ATC ATG AGG        856
AAG GCT AGT GTG CTG ATA GAA TTC CTG CTA GAT AAA TTT AAG        898
ATG AAA GAA GCA GTT ACA AGG AGT GAA ATG CTG GCA GTA GTT        940
AAC AAG AAG TAT AAG GAG CAA TTC CCT GAG ATC CTC AGG AGA        982
ACT TCT GCA CGC CTA GAA TTA GTC TTT GGT CTT GAG TTG AAG       1024
GAA ATT GAT CCC AGC ACT CAT TCC TAT TTG CTG GTA GGC AAA       1066
CTG GGT CTT TCC ACT GAG GGA AGT TTG AGT AGT AAC TGG GGG       1108
TTG CCT AGG ACA GGT CTC CTA ATG TCT GTC CTA GGT GTG ATC       1150
TTC ATG AAG GGT AAC CGT GCC ACT GAG CAA GAG GTC TGG CAA       1192
TTT CTG CAT GGA GTG GGG GTA TAT GCT GGG AAG AAG CAC TTG       1234
ATC TTT GGC GAG CCT GAG GAG TTT ATA AGA GAT GTA GTG CGG       1276
GAA AAT TAC CTG GAG TAC CGC CAG GTA CCT GGC AGT GAT CCC       1314
CCA AGC TAT GAG TTC CTG TGG GGA CCC AGA GCC CAT GCT GAA       1360
ACA ACC AAG ATG AAA GTC CTG GAA GTT TTA GCT AAA GTC AAT       1402
GGC ACA GTC CCT AGT GCC TTC CCT AAT CTC TAC CAG TTG GCT       1444
CTT AGA GAT CAG GCA GGA GGG GTG CCA AGA AGG AGA GTT CAA       1486
GGC AAG GGT GTT CAT TCC AAG GCC CCA TCC CAA AAG TCC TCT       1528
AAC ATG TAG                                                   1537
TTGAGTCTGT TCTGTTGTGT TTGAAAAACA GTCAGGCTCC TAATCAGTAG       1587
AGAGTTCATA GCCTACCAGA ACCAACATGC ATCCATTCTT GGCCTGTTAT       1637
ACATTAGTAG AATGGAGGCT ATTTTTGTTA CTTTTCAAAT GTTTGTTTAA       1687
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CTAAACAGTG CTTTTTGCCA TGCTTCTTGT TAACTGCATA AAGAGGTAAC        1737
TGTCACTTGT CAGATTAGGA CTTGTTTTGT TATTTGCAAC AAACTGGAAA        1787
ACATTATTTT GTTTTTACTA AAACATTGTG TAACATTGCA TTGGAGAAGG        1837
GATTGTCATG GCAATGTGAT ATCATACAGT GGTGAAACAA CAGTGAAGTG        1887
GGAAAGTTTA TATTGTTAAT TTTGAAAATT TTATGAGTGT GATTGCTGTA        1937
TACTTTTTTC TTTTTTGTAT AATGCTAAGT GAAATAAAGT TGGATTTGAT        1987
GACTTTACTC AAATTCATTA GAAAGTAAAT CGTAAAACTC TATTACTTTA        2037
TTATTTTCTT CAATTATGAA TTAAGCATTG GTTATCTGGA AGTTTCTCCA        2087
GTAGCACAGG ATCTAGTATG AAATGTATCT AGTATAGGCA CTGACAGTGA        2137
GTTATCAGAG TCT                                               2150


(2)  INFORMATION FOR SEQUENCE ID NO: 25:
     (i)  SEQUENCE CHARACTERISTICS:
          (A) LENGTH:  2099 base pairs
          (B) TYPE:   nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY:  linear
     (ii) MOLECULE TYPE:  genomic DNA
     (ix) FEATURE:
          (A) NAME/KEY:  smage-II
     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 25:


ACCTTATTGG GTCTGTCTGC ATATGCCTCC ACTTGTGTGT AGCAGTCTCA          50
AATGGATCTC TCTCTACAGA CCTCTGTCTG TGTCTGGCAC CCTAAGTGGC         100
TTTGCATGGG CACAGGTTTC TGCCCCTGCA TGGAGCTTAA ATAGATCTTT         150
CTCCACAGGC CTATACCCCT GCATTGTAAG TTTAAGTGGC TTTATGTGGA         200
TACAGGTCTC TGCCCTTGTA TGCAGGCCTA AGTTTTTCTG TCTGCTTAGC         250
CCCTCCAAGT GAAGCTAGTG AAAGATCTAA CCCACTTTTG GAAGTCTGAA         300
ACTAGACTTT TATGCAGTGG CCTAACAAGT TTTAATTTCT TCCACAGGGT         350
TTGCAGAAAA GAGCTTGATC CACGAGTTCG GAAGTCCTGG TATGTTCCTA         400
GAAAGATGTT CTCCTGGAAA GCTTCAAAAG CCAGGTCTCC ATTAAGTCCA         450
AGGTATTCTC TACCTGGTAG TACAGAGGTA CTTACAGGTT GTCATTCTTA         500
TCTTTCCAGA TTCCTGTCTG CCAGCTCTTT TACTTCAGCC CTGAGCACAG         550
TCAACATGCC TAGGGGTCAA AAGAGTAAGA CCCGCTCCCG TGCAAAACGA         600
CAGCAGTCAC GCAGGGAGGT TCCAGTAGTT CAGCCCACTG CAGAGGAAGC         650
AGGGTCTTCT CCTGTTGACC AGAGTGCTGG GTCCAGCTTC CCTGGTGGTT         700
CTGCTCCTCA GGGTGTGAAA ACCCCTGGAT CTTTTGGTGC AGGTGTATCC         750
TGCACAGGCT CTGGTATAGG TGGTAGAAAT GCTGCTGTCC TGCCTGATAC         800
AAAAAGTTCA GATGGCACCC AGGCAGGGAC TTCCATTCAG CACACACTGA         850
AAGATCCTAT CATGAGGAAG GCTAGTGTGC TGATAGAATT CCTGCTAGAT         900
AAGTTTAAGA TGAAAGAAGC AGTTACAAGG AGTGAAATGC TGGCAGTAGT         950
TAACAAGAAG TATAAGGAGC AATTCCCTGA GATCCTCAGG AGAACTTCTG        1000
CACGCCTAGA ATTAGTCTTT GGTCTTGAGT TGAAGGAAAT TGATCCCAGC        1050
ACTCATTCCT ATTTGCTGGT AGGCAAACTG GGTCTTTCCA CTGAGGGAAG        1100
TTTGAGTAGT AACTGGGGGT TGCCTAGGAC AGGTCTCCTA ATGTCTGTCC        1150
TAGGTGTGAT CTTCATGAAG GGTAACCGTG CCACTGAGCA AGAGGTCTGG        1200
CAATTTCTGC ATGGAGTGGG GGTATATGCT GGGAAGAAGC ACTTGATCTT        1250
TGGCGAGCCT GAGGAGTTTA TAAGAGATGT AGTGCGGGAA AATTACCTGG        1300
AGTACCGCCA GGTACCTGGC AGTGATCCCC CAAGCTATGA GTTCCTGTGG        1350
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GGACCCAGAG CCCATGCTGA AACAACCAAG ATGAAAGTCC TGGAAGTTTT          1400
AGCTAAAGTC AATGGCACAG TCCCTAGTGC CTTCCCTAAT CTCTACCAGT          1450
TGGCTCTTAG AGATCAGGCA GGAGGGGTGC CAAGAAGGAG AGTTCAAGGC          1500
AAGGGTGTTC ATTCCAAGGC CCCATCCCAA AAGTCCTCTA ACATGTAGTT          1550
GAGTCTGTTC TGTTGTGTTT GAAAAACAGT CAGGCTCCTA ATCAGTAGAG          1600
AGTTCATAGC CTACCAGAAC CAACATGCAT CCATTCTTGG CCTGTTATAC          1650
ATTAGTAGAA TGGAGGCTAT TTTTGTTACT TTTCAAATGT TTGTTTAACT          1700
AAACAGTGCT,TTTTGCCATG CTTCTTGTTA ACTGCATAAA GAGGTAACTG          1750
TCACTTGTCA GATTAGGACT TGTTTTGTTA TTTGCAACAA ACTGGAAAAC          1800
ATTATTTTGT TTTTACTAAA ACATTGTGTA ACATTGCATT GGAGAAGGGA          1850
TTGTCATGGC AATGTGATAT CATACAGTGG TGAAACAACA GTGAAGTGGG          1900
AAAGTTTATA TTGTTAGTTT TGAAAATTTT ATGAGTGTGA TTGCTGTATA          1950
CTTTTTTCTT TTTTGTATAA TGCTAAGTGA AATAAAGTTG GATTTGATGA          2000
CTTTACTCAA ATTCATTAGA AAGTAAATCA TAAAACTCTA TTACTTTATT          2050
ATTTTCTTCA ATTATTAATT AAGCATTGGT TATCTGGAAG TTTCTCCAG           2099
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(2) INFORMATION FOR SEQUENCE ID NO: 26:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acids
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr
                5

(2)   INFORMATION FOR SEQUENCE ID NO: 27
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 nucleotides
        (B) TYPE; nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27
ACTCAGCTCC TCCCAGATTT   20

(2)   INFORMATION FOR SEQUENCE ID NO: 28
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 18 nucleotides
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: cDNA
    (xi) SEQUENCE CHARACTERISTICS: SEQ ID NO: 28
TTGCCAAGAT CTCAGGAA   18

576670.1